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=> s dyad (4a) sym?
L1 2004 DYAD (4A) SYM?

=> s l1 and window
L2 5 L1 AND WINDOW

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 2 DUP REM L2 (3 DUPLICATES REMOVED)

=> d 1-2 bib ab

L3 ANSWER 1 OF 2 MEDLINE DUPLICATE 1
AN 2000013308 MEDLINE
DN 20013308 PubMed ID: 10544081
TI Requirement of replication licensing for the **dyad symmetry** element-dependent replication of the Epstein-Barr virus oriP minichromosome.
AU Shirakata M; Imadome K I; Hirai K
CS Division of Virology and Immunology, Medical Research Institute, Tokyo Medical and Dental University, Yushima 1-5-45, Tokyo, Bunkyo, 113-8510, Japan.
SO VIROLOGY, (1999 Oct 10) 263 (1) 42-54.
Journal code: 0110674. ISSN: 0042-6822.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199911
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991126
AB Latent Epstein-Barr virus genome is maintained in cells by the viral oriP-binding factor EBNA1 and cellular replication factors. EBNA1 binds to the **dyad symmetry** (DS) element in oriP and initiates DNA replication once in a single S phase, but the mechanism by which this DS-dependent replication is initiated is unknown. Replication licensing of cellular chromatins occurs during early G1 phase. Because licensing is essential for the next round of replication in S phase, it facilitates once-in-a-cell-cycle replication of the cellular genome. Using the transient replication assay with HeLa/EB1 cell, we demonstrate that the oriP plasmid required a cell cycle **window** including early G1 phase for replication in the next S phase. The plasmid containing only the DS element had a similar requirement of early G1 phase for replication. Analysis using sucrose density gradient centrifugation revealed that the oriP minichromosome existed in two distinct states: one formed at late G1 and the other formed at G2/M. These results suggest that the DS-dependent

L Number	Hits	Search Text	DB	Time stamp
1	266	dyad near4 (symmetr$3 or pair)	USPAT; US-PGPUB	2002/07/26 07:41
2	2	(dyad near4 (symmetr$3 or pair)) same window	USPAT; US-PGPUB	2002/07/26 07:42
3	4	(dyad near4 (symmetr$3 or pair)) same frequenc$3	USPAT; US-PGPUB	2002/07/26 07:43

DNA replication from oriP requires the replication licensing, implying a possible involvement of the cellular licensing factor MCM in the DNA replication from oriP.

L3 ANSWER 2 OF 2 MEDLINE DUPLICATE 2
AN 84118790 MEDLINE
DN 84118790 PubMed ID: 6546439
TI Microcomputer programs for graphic analysis of nucleic acid and protein sequences.
AU Mount D W; Conrad B
SO NUCLEIC ACIDS RESEARCH, (1984 Jan 11) 12 (1 Pt 2) 811-7.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198403
ED Entered STN: 19900319
Last Updated on STN: 19900319
Entered Medline: 19840308
AB Four computer programs are described which allow two amino acid or DNA sequences to be compared for homology, the results being displayed in a 2-dimensional array on a printer page. The programs also may be used to visualize repeated sequences or **dyad symmetry** within a DNA sequence. Two of the four programs may be used with any printer, the other two require a printer with graphics capability. Many options are available including using only a portion of a sequence, specifying a **window** to demonstrate more significant structures and special restrictions on matching such as excluding the third base in a codon. Written in the C programming language, the programs run under the CP/M 80 operating system, and may be copied in binary format through a modem. They are also available for the IBM/PC.

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 07:37:15 ON 26 JUL 2002
L1 2004 S DYAD (4A) SYM?
L2 5 S L1 AND WINDOW
L3 2 DUP REM L2 (3 DUPLICATES REMOVED)

=> s l1 and frequenc?
L4 52 L1 AND FREQUENC?

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5 20 DUP REM L4 (32 DUPLICATES REMOVED)

=> d 1-20 ti

L5 ANSWER 1 OF 20 MEDLINE DUPLICATE 1
TI Only centromeres can supply the partition system required for ARS function in the yeast Yarrowia lipolytica.

L5 ANSWER 2 OF 20 MEDLINE DUPLICATE 2
TI Structure of the mouse dipeptidyl peptidase IV (CD26) gene.

L5 ANSWER 3 OF 20 MEDLINE DUPLICATE 3
TI Transcriptional regulation by TrsN of conjugative transfer genes on

staphylococcal plasmid pGO1.

L5 ANSWER 4 OF 20 MEDLINE
TI Genetic and molecular analysis of familial isolated growth hormone deficiency.

L5 ANSWER 5 OF 20 MEDLINE DUPLICATE 4
TI Single-stranded structures are present within plasmids containing the Epstein-Barr virus latent origin of replication.

L5 ANSWER 6 OF 20 MEDLINE DUPLICATE 5
TI Characterization of the cos sites of bacteriophages P2 and P4.

L5 ANSWER 7 OF 20 MEDLINE DUPLICATE 6
TI Molecular population genetics of mtDNA size variation in crickets.

L5 ANSWER 8 OF 20 MEDLINE DUPLICATE 7
TI Plasmid deletion formation in recE4 and addB72 mutants of Bacillus subtilis.

L5 ANSWER 9 OF 20 MEDLINE DUPLICATE 8
TI Gene conversion associated with site-specific recombination in yeast plasmid pSR1.

L5 ANSWER 10 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Characterization of the genetic signals required for Epstein-Barr virus plasmid maintenance

L5 ANSWER 11 OF 20 MEDLINE DUPLICATE 9
TI Insertion of transposon Tn7 into the Escherichia coli glmS transcriptional terminator.

L5 ANSWER 12 OF 20 MEDLINE DUPLICATE 10
TI The heterochromatin of grasshoppers from the Caledia captiva species complex. I. Sequence evolution and conservation in a highly repeated DNA family.

L5 ANSWER 13 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 11
TI A PIF-DEPENDENT RECOMBINOGENIC SIGNAL IN THE MITOCHONDRIAL DNA OF YEAST.

L5 ANSWER 14 OF 20 MEDLINE DUPLICATE 12
TI Mapping genetic elements of Epstein-Barr virus that facilitate extrachromosomal persistence of Epstein-Barr virus-derived plasmids in human cells.

L5 ANSWER 15 OF 20 MEDLINE DUPLICATE 13
TI DNA sequence patterns in human, mouse, and rabbit immunoglobulin kappa-genes.

L5 ANSWER 16 OF 20 MEDLINE DUPLICATE 14
TI DNA sequence of the Escherichia coli gene, gnd, for 6-phosphogluconate dehydrogenase.

L5 ANSWER 17 OF 20 MEDLINE DUPLICATE 15
TI New approaches for computer analysis of nucleic acid sequences.

L5 ANSWER 18 OF 20 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 16
TI SEQUENCES OF BOTH TERMINI OF THE 10 GENES OF REOVIRUS SEROTYPE 3 STRAIN DEARING.

L5 ANSWER 19 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Nucleotide sequence in Xenopus 5S DNA required for transcription termination

L5 ANSWER 20 OF 20 MEDLINE DUPLICATE 17
TI Patchwork structure of a bovine satellite DNA.

=> d 17 bib ab

L5 ANSWER 17 OF 20 MEDLINE DUPLICATE 15
AN 83300027 MEDLINE
DN 83300027 PubMed ID: 6577449
TI New approaches for computer analysis of nucleic acid sequences.
AU Karlin S; Ghandour G; Ost F; Tavare S; Korn L J
NC GM10452-20 (NIGMS)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1983 Sep) 80 (18) 5660-4.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198310
ED Entered STN: 19900319
Last Updated on STN: 19970203
Entered Medline: 19831021
AB A new high-speed computer algorithm is outlined that ascertains within and between nucleic acid and protein sequences all direct repeats, **dyad symmetries**, and other structural relationships. Large repeats, repeats of high **frequency**, **dyad symmetries** of specified stem length and loop distance, and their distributions are determined. Significance of homologies is assessed by a hierarchy of permutation procedures. Applications are made to papovaviruses, the human papillomavirus HPV, lambda phage, the human and mouse mitochondrial genomes, and the human and mouse immunoglobulin kappa-chain genes.

=> d 6-10 bib ab

L5 ANSWER 6 OF 20 MEDLINE DUPLICATE 5
AN 91092507 MEDLINE
DN 91092507 PubMed ID: 2265763
TI Characterization of the cos sites of bacteriophages P2 and P4.
AU Ziermann R; Calendar R
CS Department of Molecular and Cell Biology, University of California, Berkeley 94720.
NC AI-08722 (NIAID)
SO GENE, (1990 Nov 30) 96 (1) 9-15.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M34756
EM 199102
ED Entered STN: 19910322
Last Updated on STN: 19910322
Entered Medline: 19910212
AB A 641-bp cos-containing P2 DNA fragment was sequenced and compared to the P4 cos region. Alignment of the P2 and P4 cos regions shows a homologous

region of 55 bp that has only three mismatches and contains a completely conserved region of **dyad symmetry**. A number of P4- and P2-derived cosmids were tested in an in vivo transduction assay in order to determine the minimal cos region required for packaging. These experiments show that the common region of 55 bp is sufficient for transduction with low **frequency**, but that a 125-bp cos-containing fragment contains all the information for transduction with optimal **frequency**.

L5 ANSWER 7 OF 20 MEDLINE DUPLICATE 6
AN 89232696 MEDLINE
DN 89232696 PubMed ID: 2565855
TI Molecular population genetics of mtDNA size variation in crickets.
AU Rand D M; Harrison R G
CS Department of Biology, Yale University, New Haven, Connecticut 06511.
NC GM 07499-08-10 (NIGMS)
SO GENETICS, (1989 Mar) 121 (3) 551-69.
Journal code: 0374636. ISSN: 0016-6731.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198906
ED Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890619
AB Nucleotide sequence analysis of a region of cricket (Gryllus firmus) mtDNA showing discrete length variation revealed tandemly repeated sequences 220 base pairs (bp) in length. The repeats consist of 206 bp sequences bounded by the **dyad symmetric** sequence 5'GGGGGCATGCCCCC3'. The sequence data showed that mtDNA size variation in this species is due to variation in the number of copies of tandem repeats. Southern blot analysis was used to document the **frequency** of crickets heteroplasmic for two or more different-sized mtDNAs. In New England populations of G. firmus and a close relative Gryllus pennsylvanicus approximately 60% of the former and 45% of the latter were heteroplasmic. From densitometry of autoradiographs the **frequencies** of mtDNA size classes were determined for the population samples and are shown to very different in the two species. However, in populations where hybridization between the two species has occurred, the **frequencies** of size classes and cytoplasmic genotypes in each species' distinct mtDNA lineage were shifted in a manner suggesting nuclear-cytoplasmic interactions. The data were applied to reported diversity indices and hierarchical statistics. The hierarchical statistics indicated that the greatest proportion of variation for mtDNA size was due to variation among individuals in their cytoplasmic genotypes (heteroplasmic or homoplasmic state). The diversity indices were used to estimate a per-generation mutation rate for size variants of 10(-4). The data are discussed in light of the relationship between genetic drift and mutation in maintaining variation for mtDNA size.

L5 ANSWER 8 OF 20 MEDLINE DUPLICATE 7
AN 89387439 MEDLINE
DN 89387439 PubMed ID: 2506590
TI Plasmid deletion formation in recE4 and addB72 mutants of Bacillus subtilis.
AU Peijnenburg A C; Breed P V; Bron S; Venema G
CS Department of Genetics, Center of Biological Sciences, Haren (Gn), The Netherlands.
SO PLASMID, (1989 May) 21 (3) 205-15.
Journal code: 7802221. ISSN: 0147-619X.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198910
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19891026
AB Plasmid deletion formation was compared in wild-type, recE4, and addB72 strains of Bacillus subtilis. Deletion **frequencies** in plasmid pGP1, as monitored with a penP-lacZ fusion, were low in recE4 and high in addB72, in comparison to the wild-type strain. In the wild-type and recE4 strains, deletions between directly repeated sequences were rare. In contrast, about half of the deletions in the addB72 mutant resulted from recombination at direct repeats of 5 bp or more. The sequences at or near the left deletion endpoints showed striking similarities in the three strains. (1) 5'-T-T-T-3', or the complement 5'-A-A-A-3', was frequently located at these sites. (2) 5'-T-G-T-A-3' was found close to most of these termini. (3) Nearly all left termini occurred in a region rich in hyphenated **dyad symmetry**, which includes the penP transcription/translation regulatory sequences. It is assumed that DNA secondary structures, together with a sequence preference, specify the majority of the left deletion termini, which we speculate to be target sites for topoisomerase I. The right termini of deletions in the wild-type and addB72 mutant were frequently located close to a loose octanucleotide consensus sequence: 5'-G/C-G/C-G/C-G-A/T-A/T-A/T-A/G-3'. In contrast, in the recE4 mutant, the sequence 5'-C-A-G/C-G/C-G/C-G/C-T/G-3' was more frequently found at this position.

L5 ANSWER 9 OF 20 MEDLINE DUPLICATE 8
AN 88174741 MEDLINE
DN 88174741 PubMed ID: 3280974
TI Gene conversion associated with site-specific recombination in yeast plasmid pSR1.
AU Matsuzaki H; Araki H; Oshima Y
CS Department of Fermentation Technology, Faculty of Engineering, Osaka University, Japan.
SO MOLECULAR AND CELLULAR BIOLOGY, (1988 Feb) 8 (2) 955-62.
Journal code: 8109087. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M19335; GENBANK-X02398; GENBANK-X05569
EM 198805
ED Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19880504
AB A circular DNA plasmid, pSR1, isolated from Zygosaccharomyces rouxii has a pair of inverted repeats consisting of completely homologous 959-base pair (bp) sequences. Intramolecular recombination occurs frequently at the inverted repeats in cells of Saccharomyces cerevisiae, as well as in Z. rouxii, and is catalyzed by a protein encoded by the R gene of its own genome. The recombination is, however, independent of the RAD52 gene of the host genome. A site for initiation of the intramolecular recombination in the S. cerevisiae host was delimited into, at most, a 58-bp region in the inverted repeats by using mutant plasmids created by linker insertion. The 58-bp region contains a pair with 14-bp **dyad symmetry** separated by a 3-bp spacer sequence. The recombination initiated at this site was accompanied by a high **frequency** of gene conversion (3 to 50% of the plasmid clones examined). Heterogeneity created by the linker insertion or by a deletion (at most 153 bp so far tested) at any place on the inverted repeats was converted to a homologous

combination by the gene conversion, even in the rad52-1 mutant host. A mechanism implying branch migration coupled with DNA replication is discussed.

L5 ANSWER 10 OF 20 CAPLUS COPYRIGHT 2002 ACS
AN 1987:97026 CAPLUS
DN 106:97026
TI Characterization of the genetic signals required for Epstein-Barr virus plasmid maintenance
AU Lupton, Stephen; Levine, A. J.
CS Dep. Mol. Biol., Princeton Univ., Princeton, NJ, 08544, USA
SO Cancer Cells (1986), 4(DNA Tumor Viruses: Control Gene Expression Replication), 543-53
CODEN: CACEEG; ISSN: 0743-2194
DT Journal
LA English
AB The Epstein-Barr virus (EBV) genome becomes established as a multicopy plasmid in the nucleus of infected B lymphocytes. A cis-acting DNA sequence discovered within the BamHI-C fragment of the EBV genome allows stable extrachromosomal plasmid maintenance in latently infected cells, but not in EBV-neg. cells. Deletion anal. assigned this function to a 2208-bp region of the BamHI-C fragment contg. a striking repetitive sequence and a large **dyad symmetry**. A recombinant vector, p410+, was constructed that carries the BamHI-K fragment, encoding the EBV-assocd. nuclear antigen (EBNA-1), the cis-acting sequence from the BamHI-C fragment, and a dominant, selectable marker gene. After transfection of HeLa cells, this plasmid conferred G418 resistance (G418r) and persisted extrachromosomally. Mutations in the BamHI-K-derived portion of p410+, altering the carboxyterminal portion of EBNA-1, destroyed the ability of the plasmid to persist extrachromosomally in HeLa cells. These observations indicate that in combination with the cis-acting sequence located in the BamHI-C fragment, EBNA-1 is in part responsible for EBV-derived extrachromosomal plasmid maintenance in HeLa cells. Deletion mapping demonstrated that a portion of the BamHI-C fragment can functionally substitute for the SV40 enhancer and promoter. The enhanced **frequency** of G418r colonies formed by some EBV-derived plasmids when introduced into D98-Raji cells did not correlate with the ability to be maintained extrachromosomally. One interpretation of these data is that the BamHI-C fragment contains a promoter element stimulated by an EBV- or lymphocyte-induced gene function.

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 07:37:15 ON 26 JUL 2002

L1 2004 S DYAD (4A) SYM?
L2 5 S L1 AND WINDOW
L3 2 DUP REM L2 (3 DUPLICATES REMOVED)
L4 52 S L1 AND FREQUENC?
L5 20 DUP REM L4 (32 DUPLICATES REMOVED)

US-PAT-NO: 5356796

DOCUMENT-IDENTIFIER: US 5356796 A

TITLE: Repressor protein and operon for regulating expression of polypeptides
and its use in the preparation of 2,2-dialkyglycine decarboxylase of
Pseudomonas cepacia

---------- KWIC ---------

Identification of Operator--Candidate repressor binding sites O1 and O2, (FIG.
17) were located by dot matrix analysis of the sequence of the 788 bp PCR
fragment in which the sequence of one strand was aligned with its reverse
complement and sequence identities within a 12-nucleotide window were
determined. No sequences with dyad symmetry were found in the intergenic
region, but two regions with strong dyad symmetry were found in the adjacent
genes: O1, 335 bp into the decarboxylase gene, and O2, 76 bp into the repressor
gene.